AMENDMENTS TO THE CLAIMS

This listing of the claims will replace all prior versions, and listings, of claims in this application.

Listing of Claims:

1-48. Canceled

49. (Currently Amended) A method of diagnosing Hepatitis C virus (HCV) infection, comprising contacting an isolated, purified, or synthetic polypeptide comprising an amino acid sequence of at least 8 amino acids in length which amino acid sequence is encoded by an HCV nucleic acid molecule comprising a nucleotide sequence corresponding to SEQ ID NO:1 and translated in a reading frame corresponding to the reading frame of SEQ ID NO:1 and +1 to the standard HCV reading frame with a biological sample from a subject, under conditions where the polypeptide and an antibody that binds to the polypeptide present in the sample can bind, and determining the presence or absence of the antibody, wherein presence of the antibody indicates infection with HCV.

50. (Previously Presented) The method of claim 49, wherein the amino acid sequence is at least 14 amino acids in length.

51. (Previously Presented) The method of claim 49, wherein the amino acid sequence is at least at least 30 amino acids in length.

52. (Previously Presented) The method of claim 49, wherein the amino acid sequence is at least 100 amino acids in length.

53. (Previously Presented) The method of claim 49, wherein the entire polypeptide is encoded by a reading frame +1 to the standard hepatitis C reading frame.

54. (Previously Presented) The method of claim 49, wherein the amino acid sequence comprises at least 8 contiguous amino acids of SEQ ID NO:2.

55. (Previously Presented) The method of claim 49, wherein the amino acid sequence is identical to the amino acid sequence shown in SEQ ID NO:2.

56. (Previously Presented) The method of claim 49, wherein the amino acid sequence comprises at least 8 contiguous amino acids of SEQ ID NO:9.

57. (Previously Presented) The method of claim 49, wherein the amino acid sequence is selected from the group consisting of: SEQ ID NO: 3, SEQ ID NO:4, SEQ ID NO:5, and SEQ ID NO:6.

58. (Previously Presented) The method of claim 49, wherein the amino acid sequence is selected from the group consisting of: LNLKEKP(X1)(X2)TPT(X3) (SEQ ID NO:3) and AAHRT(X4)SSR(X5)(X6)VR (SEQ ID NO:4) , wherein X1 is N or K, X2 is V or E, X3 is A or V, X4 is L or S, X5 is A or V, and X6 is A or V.

59. (Previously Presented) The method of claim 49, wherein the amino acid sequence is selected from the group consisting of: LNLKEKPNVTPTA (SEQ ID NO:5) and AAHRTSSSRAVVR (SEQ ID NO:6).

60. (Previously Presented) The method of claim 49, wherein the polypeptide is a fusion protein.

61. (Currently Amended) The method of claim 49, wherein translation of the polypeptide begins at the initiation site of the standard HCV ~~HCF~~ open reading frame with a shift into the +1 reading frame.

62. (Previously Presented) The method of claim 49, wherein an enzyme-linked immunosorbent assay (ELISA) assay is used to detect a binding antibody in the biological sample.

63. (Previously Presented) The method of claim 49, wherein an radioimmunoassay (RIA) is used to detect a binding antibody in the biological sample.

64. (Previously Presented) The method of claim 49, wherein an western blot assay is used to detect a binding antibody in the biological sample.

65. (Previously Presented) The method of claim 49, wherein the polypeptide is immobilized on a surface.

66. (Previously Presented) The method of claim 49, wherein the polypeptide is supplied in a kit.

67. (Currently Amended) A method of diagnosing Hepatitis C virus (HCV) infection, comprising contacting an isolated, purified, or synthetic polypeptide comprising an amino acid sequence of at least 8 amino acids in length which amino acid sequence is encoded by an HCV nucleic acid molecule ~~which amino acid sequence is encoded by a nucleic acid molecule~~ comprising a nucleotide sequence shown in SEQ ID NO:1 and translated in a reading frame +1 to the standard HCV reading frame with a biological sample from a subject, under conditions where the polypeptide and an antibody that binds to the polypeptide present in the sample can bind, and determining the presence or absence of the antibody wherein presence of the antibody indicates infection with HCV.

68. (Previously Presented) The method of claim 67, wherein the amino acid sequence is at least 14 amino acids in length.

69. (Previously Presented) The method of claim 67, wherein the amino acid sequence is at least at least 30 amino acids in length.

70. (Previously Presented) The method of claim 67, wherein the amino acid sequence is at least 100 amino acids in length.

71. (Previously Presented) The method of claim 67, wherein the entire polypeptide is encoded by a reading frame +1 to the standard hepatitis C reading frame.

72. (Previously Presented) The method of claim 67, wherein the amino acid sequence comprises at least 8 contiguous amino acids of SEQ ID NO:2.

73. (Previously Presented) The method of claim 67, wherein the amino acid sequence is identical to the amino acid sequence shown in SEQ ID NO:2.

74. (Previously Presented) The method of claim 67, wherein the amino acid sequence comprises at least 8 contiguous amino acids of SEQ ID NO:9.

75. (Previously Presented) The method of claim 67, wherein the amino acid sequence is selected from the group consisting of: SEQ ID NO: 3, SEQ ID NO:4, SEQ ID NO:5, and SEQ ID NO:6.

76. (Previously Presented) The method of claim 67, wherein the amino acid sequence is selected from the group consisting of: LNLKEKP(X1)(X2)TPT(X3) (SEQ ID NO:3) and AAHRT(X4)SSR(X5)(X6)VR (SEQ ID NO:4) , wherein X1 is N or K, X2 is V or E, X3 is A or V, X4 is L or S, X5 is A or V, and X6 is A or V.

77. (Previously Presented) The method of claim 67, wherein the amino acid sequence is selected from the group consisting of: LNLKEKPNVTPTA (SEQ ID NO:5) and AAHRTSSSRAVVR (SEQ ID NO:6).

78. (Previously Presented) The method of claim 67, wherein the polypeptide is a fusion protein.

79. (Currently Amended) The method of claim 67, wherein translation of the polypeptide begins at the initiation site of the standard HCV ~~HCF~~ open reading frame with a shift into the +1 reading frame.

80. (Previously Presented) The method of claim 67, wherein an enzyme-linked immunosorbent assay (ELISA) assay is used to detect a binding antibody in the biological sample.

81. (Previously Presented) The method of claim 67, wherein an radioimmunoassay (RIA) is used to detect a binding antibody in the biological sample.

82. (Previously Presented) The method of claim 67, wherein an western blot assay is used to detect a binding antibody in the biological sample.

83. (Previously Presented) The method of claim 67, wherein the polypeptide is immobilized on a surface.

84. (Previously Presented) The method of claim 67, wherein the polypeptide is supplied in a kit.

85. (Currently Amended) A method of diagnosing Hepatitis C virus (HCV) infection, comprising contacting an isolated, purified, or synthetic polypeptide comprising an amino acid sequence of at least 8 amino acids in length which amino acid sequence is encoded by an HCV nucleic acid molecule comprising a nucleotide sequence corresponding to SEQ ID NO:1 and translated in a reading frame corresponding to the reading frame of SEQ ID NO:1 and +1 to the standard HCV reading frame, which polypeptide is immobilized on a surface, with a biological sample from a subject, under conditions where the polypeptide and an antibody that binds to the polypeptide can bind, determining the presence or absence of an antibody that binds to the polypeptide, wherein the presence or absence of the antibody is detected using a secondary antibody or fragment thereof which is detectably labeled, and wherein presence of the antibody indicates infection with HCV.

86. (Previously Presented) The method of claim 85, wherein an enzyme-linked immunosorbent assay (ELISA) assay is used to detect a binding antibody in the biological sample.

87. (Previously Presented) The method of claim 85, wherein an radioimmunoassay (RIA) is used to detect a binding antibody in the biological sample.

88. (Previously Presented) The method of claim 85, wherein an western blot assay is used to detect a binding antibody in the biological sample.

89. (Previously Presented) The method of claim 85, wherein the immobilized polypeptide is supplied in a kit.

90. (Previously Presented) A kit for diagnosing Hepatitis C virus (HCV) infection, comprising an isolated, purified, or synthetic polypeptide comprising an amino acid sequence of at least 8 amino acids in length which amino acid sequence is encoded by an HCV nucleic acid molecule comprising a nucleotide sequence corresponding to SEQ ID NO:1 and translated in a reading frame corresponding to the reading frame of SEQ ID NO:1 and +1 to the standard HCV reading frame, which polypeptide is immobilized on a surface.

91. (Currently Amended) The kit for of claim 90, further comprising a secondary anti-human antibody ~~ntibody~~ which is detectably labeled.